Li Y, Hui G, Yu S, Luo Y, Yao X, Ye S (2017).
Nearest neighbour relationships in Pinus yunnanensis var. tenuifolia forests along the Nanpan River, China
iForest – Biogeosciences and Forestry – doi: 10.3832/ifor2405-010

Supplementary Material

Fig. S1 - Pearson's correlation coefficient for M in the M–U joint distribution. The lower triangle shows the correlation coefficient; circle color indicates a positive/negative value between the tested variables, and circle size shows the degree of correlation. Where (×) indicates $p > 0.005$ (no significant correlation) and circles without (×) indicate a significant correlation ($p < 0.005$).

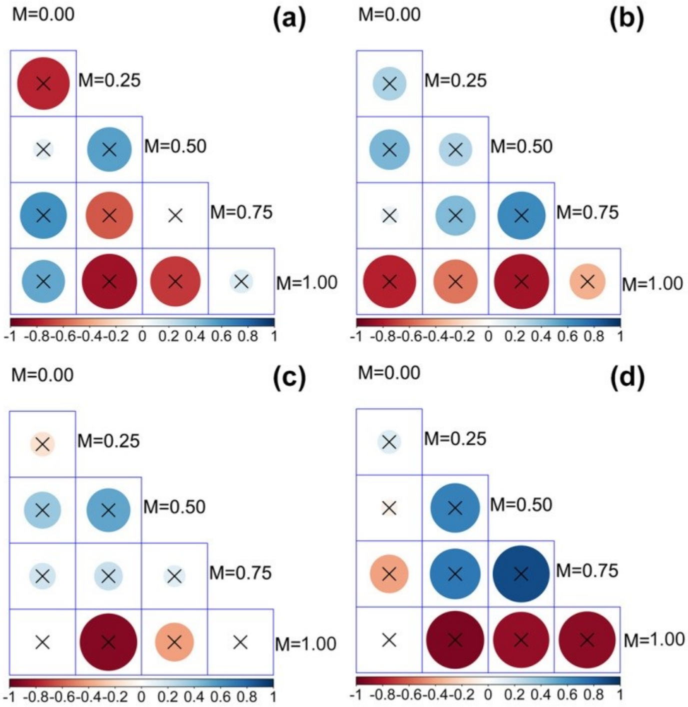


Fig. S2 - Spearman's rank correlation coefficient for dominance (U) in the M–U joint distribution. Details as in Fig. S1.

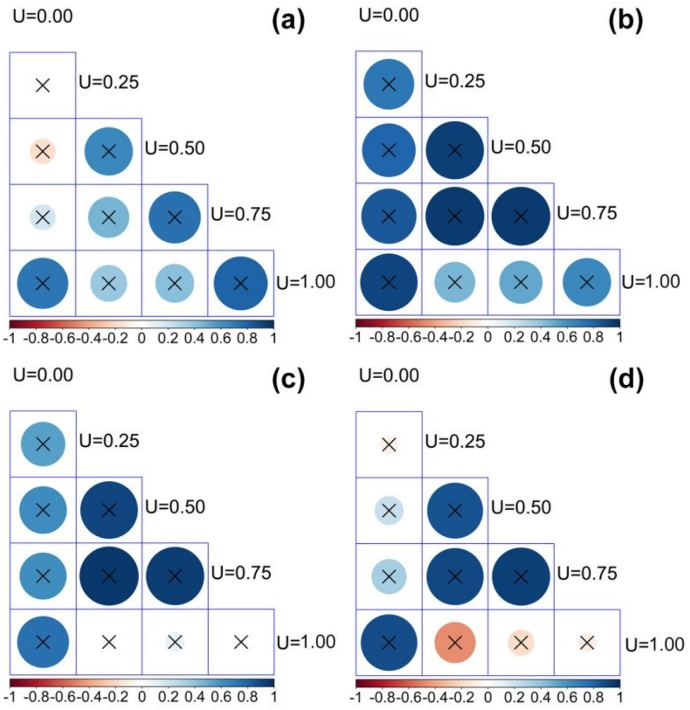


Fig. S3 - Spearman’s rank correlation coefficient for mingling (M) in the M–W joint. Details as in Fig. S1.

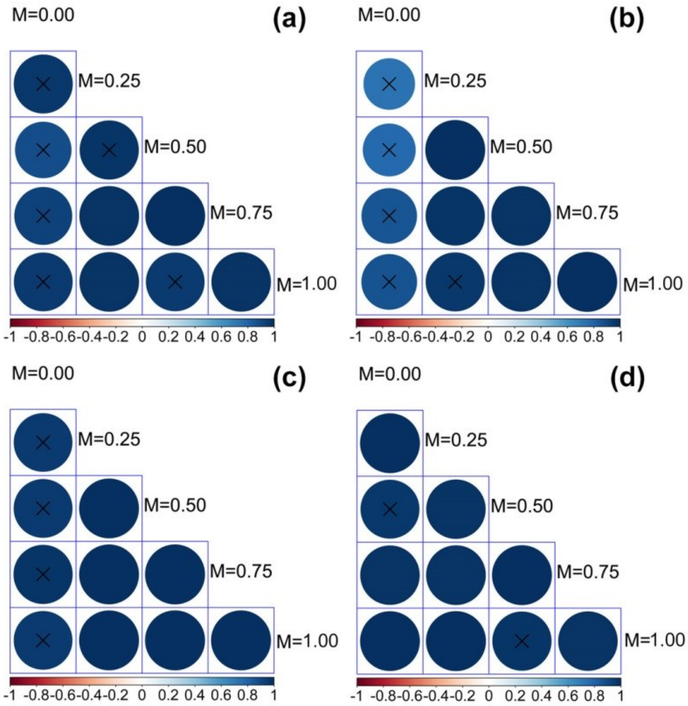


Fig. S4 - Spearman's rank correlation coefficient for uniform angle index (W) in the M–W joint distribution. Details as in Fig. S1.

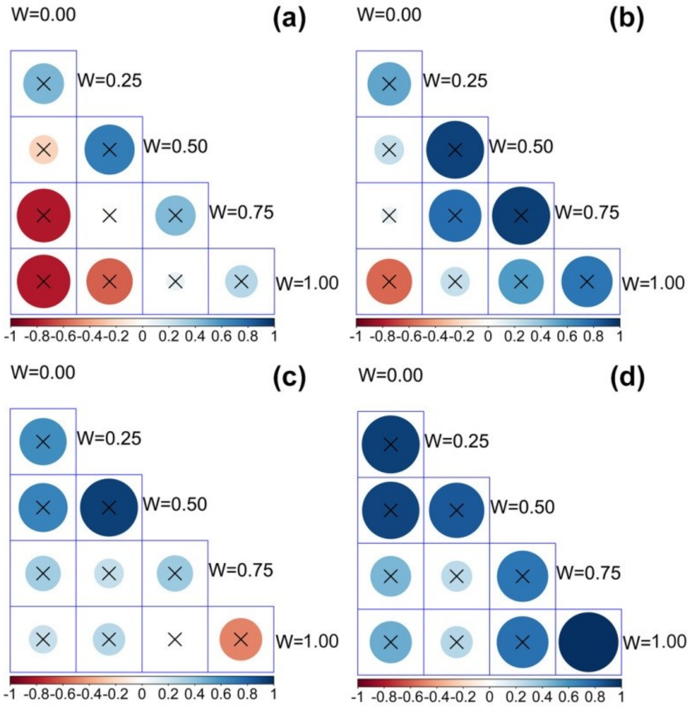


Fig. S5 - Spearman's rank correlation coefficient of dominance (U) in the U–W joint distribution. Details are as in Fig. S1.

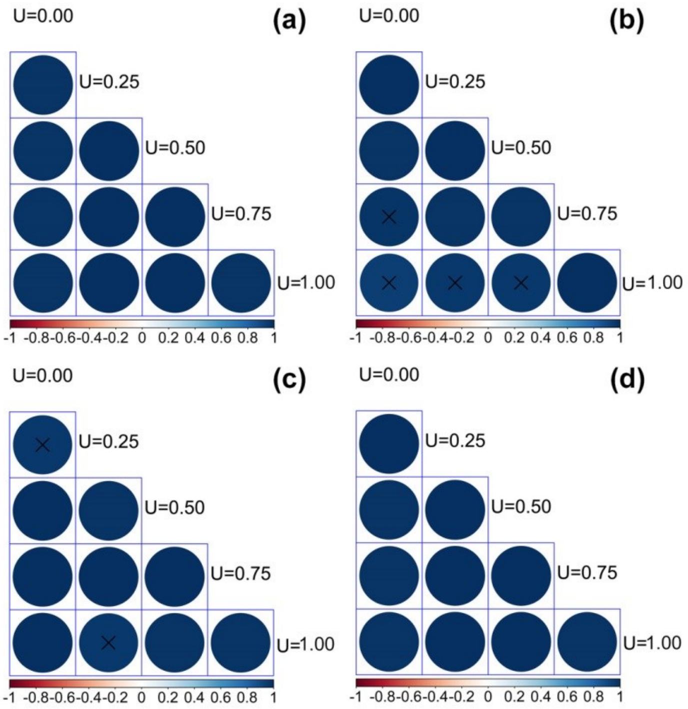
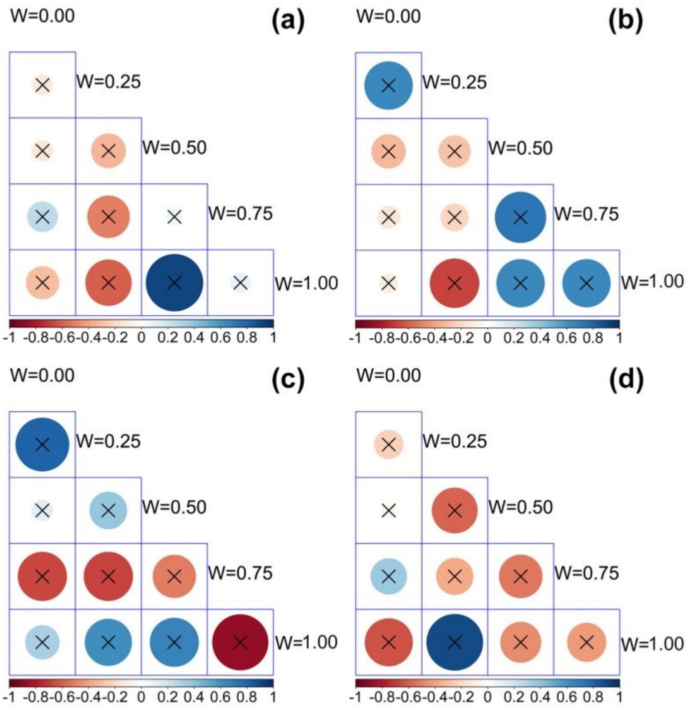


Fig. S6 - Spearman’s rank correlation coefficient of uniform angle index (W) in U–W joint distribution. Details are as in Fig. S1.



Box 1 - R code calculated four nearest neighbor structure indices: Mingling, Symmetry, Dominance, was provided by Zhang GongQiao, Hui Ganging, Zhao ZhongHua, Klaus v. Gadow and Yuanfa Li. 2014, (Unpublished).

```
# Functions (most of the programming by Zhang GongQiao & K. Gadow, 2014)
# Find the 4 nearest neighbors for 1 tree (Zhang GongQiao)
Near.f=function(x0,y0,data1){
   x1=abs(data1$x-x0); y1=abs(data1$y-y0)
   dis=sqrt(x1*x1+y1*y1); nord=order(dis); nord[1:5]
data2=rbind(data1[nord[1],],data1[nord[2],],data1[nord[3],],data1[nord[4],],data1[nord[5],])
}
# Mingling for one tree (Zhang GongQiao)
Ming.f<-function (sp0,spNB){
count<-0 ; for (i in 1:4) { if (! identical(sp0,spNB[i])) count<-count+1}
m<-count/4}
# Dominance for one tree (Zhang GongQiao; KG)
Dom.f<-function (D0,hNB){
count<-0; for (i in 1:4){if (hNB[i]<=D0) count<-count+1}
u<-count/4}
# Symmetry for one tree (Zhang GongQiao)
# Calculate the angle between two trees
Angle.f=function(x0,y0,xi,yi){
  deltax=xi-x0; deltay=yi-y0
  if (deltay>0 &deltax>=0) {Angle=atan(deltax/deltay)} else
  if (deltay==0 &deltax>=0) {Angle=pi*0.5} else
  if (deltay<=0 &deltax>=0) {Angle=pi+atan(deltax/deltay)} else
  if (deltay<0 &deltax<0) {Angle=pi+atan(deltax/deltay)} else
  if (deltay==0 &deltax<0) {Angle=pi*1.5} else
  {Angle=pi*2+atan(deltax/deltay)}
  Angle
}
# Calculate the difference of two angles & compare to 72°
AngleDiff.f=function(Angle1,Angle2){
  AngleDiff=Angle1-Angle2
  if (AngleDiff>pi) {AngleDiff=2*pi-AngleDiff}
  if (AngleDiff>=72*pi/180){AngleDiff=0} else
  {AngleDiff=1}
}
# calculate Angle Index for one tree
W.f=function(x0,y0,x,y){
  Angle4=c()
  for(i in 1:4){
    xi=x[i];yi=y[i]
    Angle4[i]=Angle.f(x0,y0,xi,yi)
  }
  Angle4o=order(Angle4)
  count12=AngleDiff.f(Angle4[Angle4o[2]],Angle4[Angle4o[1]])
  count23=AngleDiff.f(Angle4[Angle4o[3]],Angle4[Angle4o[2]])
  count34=AngleDiff.f(Angle4[Angle4o[4]],Angle4[Angle4o[3]])
  count41=AngleDiff.f(Angle4[Angle4o[4]],Angle4[Angle4o[1]])
  count=(count12+count23+count34+count41)/4
  w=count
}
# Implementing the Structure Functions
# define ref trees: species and plot
dat<-datRA4; specie="Guarea macrophylla" # dat<-datRB1;dat<-datT7;
marg<-5                              # margin
y1<-max(dat$y)-marg; y2<-min(dat$y)+marg; x1<-max(dat$x)-marg; x2<-min(dat$x)+marg
reftree<-subset(dat, dat$sp==specie&dat$x>x2&dat$x<x1&dat$y>y2&dat$y<y1)
```

```
# Calculations

M <-array(NA); D <-array(NA); W <-array(NA); C<-array(NA); T<-array(NA)

for (i in 1:length(reftree$x)){
  x0=reftree[i,]$x;y0= reftree[i,]$y
  Near4=Near.f(x0,y0, dat)[2:5,]         # dataframe NB's for 1 reftree
  x=Near4$x; y=Near4$y              # coordinates ref tree and neighbors
  W[i]=W.f(x0,y0,x,y)                #function Aggregation
  sp0=reftree[i,]$sp; spNB=Near4$sp
  M[i]=Ming.f(sp0,spNB)              #function Mingling
  d0=reftree[i,]$d1; d=Near4$d1
  D[i]=Dom.f(d0,d)                  #function Dominance
  cr0=reftree[i,]$cr; crNB=Near4$cr
  C[i]<-Cr.f(x0,y0,x,y,cr0,crNB)          #function Crowding
  t0=c(reftree[i,]$d1, tNB=Near4$d1)
  T[i]=sqrt(var(t0))/mean(t0); if(T[i]>1) T[i]<-1 # dbh differentiation
}
  reftree$Sp=specie; reftree$M=M; reftree$D=D; reftree$W=W; reftree$C=C; reftree$T=T
  reftree
```